

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Patricia D. Murphy)
Application No.: 09/923,327) Group Art Unit: 1634
Filed: August 8, 2001) Examiner: Stephanie W. Zitomer, Ph.D.
For: Determining common functional alleles in a population and uses therefor)))
Commissioner for Patents U.S. Patent and Trademark Office 2011 South Clark Place Customer Window, Mail Stop SEQUENCE Crystal Plaza Two, Lobby, Room 1B03 Arlington, VA 22202	E
STATEMENT ACCOMPANYIN	NG SUBSTITUTE SEQUENCE LISTING
The undersigned hereby states upon	information and belief that the Substitute Sequence
Listing submitted herewith does not include	matter which goes beyond the content of the
application as filed and that the information	recorded on the diskette submitted herewith is
identical to the written Substitute Sequence	Listing submitted concurrently herewith. This
Substitute Sequence Listing is responsive to	an Office Action dated June 17, 2003 (paper no. 6-
13).	
•	Respectfully submitted, MORGAN, LEWIS & BOCKIUS LLP
	By: <u>Mosanne Kosson</u> Rosanne Kosson Reg. No. 46,840
Customer No. 009629 MORGAN, LEWIS & BOCKIUS LLP 1111 Pennsylvania Ave., NW Washington, D.C. 20004 Tel: 202-739-3000: Fax: 202-739-3001	



it is		
7 2003 H		
	SEQUENCE LISTING	
EMAT10>	MURPHY, Patricia D.	
<120>	Determining Common Functional Alleles in a Population and Uses Therefor	
<130>	044921-5054-02	
	US 09/923,327 2001-08-08	
	US 08/598,591 1996-02-12	
	US 08/798,691 1997-02-12	
	US 08/905,772 1997-08-04	
	US 09/084,471 1998-03-22	
	US 09/129,134 1998-08-04	
	US 09/524,794 2000-03-14	
<160>	262	
<170>	PatentIn version 3.1	
<212>	1 19 DNA Homo sapiens	
<400> cgcgtc	1 tgct tatgattgg	19
<210><211><211><212>		
<213> <400> tctctg	Homo sapiens 2 aggc gggaaagg	18

<210> 3 <211> 20 <212> DNA <213> Homo sapiens

<400> 3 ttttttttt tttaaggagc .	20
<210> 4 <211> 21 <212> DNA <213> Homo sapiens	
<400> 4 cacattttta tttttctact c	21
<210> 5 <211> 20 <212> DNA <213> Homo sapiens	
<400> 5 gcttataaaa ttttaaagta	20
<210> 6 <211> 19 <212> DNA <213> Homo sapiens	
<400> 6 ctggaatctc ctctatcac	19
<210> 7 <211> 23 <212> DNA <213> Homo sapiens	
<400> 7 ttcatttttg cttttcttat tcc	23
<210> 8 <211> 20 <212> DNA <213> Homo sapiens	
<400> 8 atatgacaga aatatccttc	20
<210> 9 <211> 21 <212> DNA <213> Homo sapiens	
<400> 9 cagtggtata gaaatcttcg a	21

<210> <211> <212>	10 20 DNA	
	Homo sapiens	
<400>	10	20
tttttt	ttt ttttacctga	20
<210>	11	
<211>	20	
	DNA	
<213>	Homo sapiens	
	11	20
actaatç	gage ttgccattet	20
<210>	12	
	19	
	DNA	
<213>	Homo sapiens	
<400>	12	10
tgggtaa	actg caggttaca	19
<210>	13	
<211>	18	
	DNA	
<213>	Homo sapiens	
<400>	13	
gactta	cgtg cttagttg	18
<210>	14	
<211>	24	•
<212>	DNA	
<213>	Homo sapiens	
<400>	14	24
agtatat	catt gtatgagttg aagg	24
<210>	15	
<211>	25	
<212>	DNA	
<213>	Homo sapiens	
<400>	15	
gatttgi	tatt ctgtaaaatg agatc	25
<210>	16	
<211>	23	

<212> DNA <213> Homo sapiens	
<400> 16 ggcctttgct ttttaaaaat aac	2
<210> 17	
<211> 22	
<212> DNA <213> Homo sapiens	
22133 HOMO BAPTOTT	
<400> 17	:
gtctttaccc attatttata gg	
<210> 18	
<211> 22	
<212> DNA <213> Homo sapiens	
<213> NOMO Baprome	
<400> 18 gtatagacaa aagaattatt cc	
<210> 19	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 19	
ggtagtaggt atttatggaa tac	
<210> 20	
<211> 19	
<212> DNA	
<213> Homo sapiens	•
<400> 20	
catgttagag catttaggg	
<210> 21	
<211> 19	
<212> DNA <213> Homo sapiens	
<213> Homo sapiens	
<400> 21	
cacattgctt ctagtacac	
<210> 22	
<211> 18	
<212> DNA <213> Homo sapiens	

<400> 22	
ccaggtgaca ttcagaac	18
<210> 23	
<211> 19	
<212> DNA	
<213> Homo sapiens	
AZISS NOME DIPLOM	
<400> 23	
	19
attcagtatt cctgtgtac	19
<210> 24	
<211> 17	
<212> DNA	
<213> Homo sapiens	
<400> 24	
	17
cgttaccccc acaaagc	L /
<210> 25	
<211> 20	
<212> DNA	
<213> Homo sapiens	
•	
<400> 25	
	20
atgetatget agegeaaace	
<210> 26	
<211> 20	
<212> DNA	
<213> Homo sapiens	
<400> 26	
	20
Cononggana democrace	
210. 27	
<210> 27	
<211> 20	
<212> DNA	
<213> Homo sapiens	
<400> 27	
taccacattt tatgtgatgg	20
3 3 33	
<210> 28	
<211> 17	
<212> DNA	
<213> Homo sapiens	
<400> 28	
ggggtagtaa gtttccc	17

<210>	29	
<211>	18	
<212>	DNA	
<213>	Homo sapiens	
<400>	29	
ctcttc	tcat gctgtccc	18
<210>	30	
<211>		
<212>		
<213>	Homo sapiens	
<400>	30	0.0
atagaga	aagc taagttaaac	20
.212	21	
<210>		
<211>		
<212>		
<213>	Homo sapiens	
.400		
<400>	31	20
Ladila	ctca tgggacattc	20
<210>	32	
<211>		
<212>		
	Homo sapiens	
12137	nomo bupitens	
<400>	32	
	gaca gttaacacta	20
J J	J	
<210>	33	
<211>		
<212>		
<213>	Artificial sequence	
<220>		
<223>	M13 tail for forward primers	
<400>	33	
tgtaaa	acga cggccagt	18
<210>	34	
<211>	18	
<212>		
<213>	Artificial sequence	
000		
<220>	Na 1 17 6	
<223>	M13 tail for reverse primers	

<400>	34	
	aacag ctatgacc	18
cayyaa	acay cracyacc	10
<210>		
<211>		
<212>	DNA	
<213>	Homo sapiens	
<400>	35	
aggcac	tgag gtgattggc	19
<210>	36	
<211>		
<212>		
<213>	Homo sapiens	
<400>	76	
		19
Legtag	gccct taagtgagc	13
010		
<210>		
<211>		
<212>		
<213>	Homo sapiens	
<400>		
tgaggc	cacta ttgtttgtat tt	22
<210>	38	
<211>		
<212>		
	Homo sapiens	
-213/	nomo papiono	
<400>	3.8	
		22
rgrryg	stgtt gaatttttca gt	44
-010-	20	
<210>		
<211>		
<212>		
<213>	Homo sapiens	
<400>		
agagat	ttgg aaaatgagta ac	22
<210>	40	
<211>		
<212>		
	Homo sapiens	
/	nome papatiti	
<400>	40	
	gtcat cacaggagg	19
acaacy	,	

<210> <211> <212>	41 18 DNA	
	Homo sapiens	
<400>	41 gaca gtgggtga	18
5 55 .		
<210>	42	
<211>		
<212> <213>	DNA Homo sapiens	
<400>	42 tetg agacetagge	20
J		
<210>	43	
	22	
<212>		
<213>	Homo sapiens	
	43	
gatttt	ctet ttteeeettg gg	22
<210>		
<211>		
<212>		
<213>	Homo sapiens	
<400>	44	
caaacaa	aagc ttcaacaatt tac	23
<210>	45	
<211>	26	
<212> <213>	DNA Homo sapiens	
(213)	nomo saprens	
<400>	45	26
gggttt	tatt ttcaagtact tctatg	26
-210-	46	
<210> <211>		
<211>		
	Homo sapiens	
<400>	46	
	caac tgttcaatgt atgagc	26
, ,		
<210>	47	
<211>		

<212> <213>	DNA Homo sapiens	
<400>	47	
ctagtgt	tgtg tttttggc	18
<210>	48	
<211>		
<212>		
	Homo sapiens	
<400>	48	
cataac	etta tetecace	18
	49	
<211>	23	
<212>		
<213>	Homo sapiens	
<400>	49	
	catg agacaataaa tcc	23
cccago	agabaabaaa too	
<210>	50	
<211>	21	
<212>		
<213>	Homo sapiens	
400	50	
<400>	50	21
ggttee	caaa taatgtgatg g	21
<210>	51	
<211>	21	
<212>	DNA	
<213>	Homo sapiens	
<400>	51	
gtttat	ggga aggaaccttg t	21
<210>	52	
<211>	21	
<212>		
<213>	Homo sapiens	
	• • • • • • • • • • • • • • • • • • • •	
<400>	52	
tggtcc	cata aaattccctg t	21
011	50	
<210>	53	
<211> <212>	24 DNA	
	Homo sapiens	
~~ ~ ~ /	nome petrane	

<400> 53 catgactttg tgtgaatgta cacc	24
<210> 54 <211> 24 <212> DNA <213> Homo sapiens	
<400> 54 gaggagagcc tgatagaaca tctg	24
<210> 55 <211> 20 <212> DNA <213> Homo sapiens	
<400> 55 gggctttttc tccccctccc	20
<210> 56 <211> 18 <212> DNA <213> Homo sapiens <400> 56 aaaatctggg ctctcacg	18
<210> 57 <211> 20 <212> DNA <213> Homo sapiens <400> 57 tttaatacag actttgctac	20
<210> 58 <211> 20 <212> DNA <213> Homo sapiens <400> 58 gaaaagccaa agttagaagg	20
<210> 59 <211> 20 <212> DNA <213> Homo sapiens <400> 59 tgcaacccac aaaatttggc	20

	60	
<211>	20	
<212>	DNA	
	Homo sapiens	
<400>	60	
	cat ttccaaaacc	2
	cat ttccaaaacc	-
<210>	61	
	18	
<212>		
<213>	Homo sapiens	
	61	٦,
tggtgtc	tct agttctgg	1
-210-	60	
	62 20	
<212>		
<213>	Homo sapiens	
-100-	62	
	62	2
cattget	gta gtagctctgc	۱ ک
<210>	63	
	21	
<212>		
<213>	Homo sapiens	
-4.00	52	
	63	2
gcagaac	tat gtctgtctca t	2
<210>	64	
	19	
	DNA	
<213>	Homo sapiens	
-100-	64	
<400>		1.
cygreag	ttg aaatgtcag	1
<210>	65	
	19	
	DNA	
<213>	Homo sapiens	
	65	_
catttgg	atc cgttaaagc	1
010		
	66	
<211>	23	

<212> <213>	DNA Homo sapiens	
1227		
<400>	66	
cacccgg	gctg gaaattttat ttg	23
<210>	67	
<211>		
<212>	·	
<213>	Homo sapiens	
<400>	67	
ggaaagg	gcac tggagaaatg gg	22
<210>	68	
	25	
<212>		
	Homo sapiens	
<400>	68	
ccctcca	agca cacatgcatg taccg	25
<210>	69	
	20	
<212>		
	Homo sapiens	
<400>	69	
taagtag	gtct gtgatctccg	20
<210>	70	
<211>	18	
	AND	
<213>	Homo sapiens	
<400>	70	
atgtate	gagg teetgtee	18
<210>	71	
<211>	18	
<212>	DNA	
<213>	Homo sapiens	
<400>	71	
gacacca	agtg tatgttgg	18
<210>	72	
<211>	20	
<212>	DNA	
<213>	Homo sapiens	

<400> gagaaa	72 gaag aacacatccc	20
<210>	73	
<211>	24	
<212>		
<213>	Homo sapiens	
<400>	73	
gaagtt	gtca ttttataaac cttt	24
510		
<210>	74	
<211> <212>	22	
<213>	Homo sapiens	
<400>	74 ttct tccctagtat gt	22
090000		
<210>	75	
<211>	20	
<212>	DNA	
<213>	Homo sapiens	
<400>	75	
tcctga	caca gcagacatta	20
<210>	76	
<211>	20	
<212>	DNA	
<213>	Homo sapiens	
<400>	76	
ttggat	ttcg ttctcactta	20
<210>	77	
<211>	20	
<212>	DNA	
<213>	Homo sapiens	
<400>	77	
ctctta	aggg cagttgtgag	20
<210>	78	
<211>	20	
<212>	DNA	
<213>	Homo sapiens	
<400>	78	
	ctat gattacttcc	20

<210>	79		
<211>	23		
<212>	DNA		
<213>	Homo sapiens		
	L		
<400>	79		
	tag tgtccttaaa	agg	23
cccacc	.cug cgccccaua	~	
<210>	80		
<211>	22		
<212>	DNA		
<213>	Homo sapiens		
<400>	80		
tttcato	gac agcacttgag	ta	22
	,55	· 3	
<210>	81		
<211>			
<212>			
<213>	Homo sapiens		
<400>	81		
cacaaca	aag agcatacata	ggg	23
<210>	82		
<211>			
<212>			
<213>	Homo sapiens		
<400>	82		
tcgggtt	cac tctgtagaag		20
<210>	83		
<211>	21		
<212>			
	Homo sapiens		
<400>	83		
	cag gaggaaaagc		21
	.cay gaggaaaagc	a	۷ 1
010	^4		
<210>	84		
<211>	21		
<212>	DNA		
<213>	Homo sapiens		
<400>	84		
gctgcct	acc acaaatacaa	a	21
-			
<210>	85		
. 7.7.7.	0.1		

<212> <213>	DNA Homo sapiens	
<400> ccacag	85 taga tgctcagtaa a	21
<210>	86	
<211>		
<212>		
<213>	Homo sapiens	
<400>	86	
taggaa	aata ccagcttcat aga	23
<210>	87	
<211>	20	
<212>		
<213>	Homo sapiens	
<400>	87	
	gctt tctgtaatcg	20
<210>	88	
<211>		
<212>		
<213>	Homo sapiens	
<400>	88	
gtatct	accc actctcttct tcag	24
<210>	89	
<211>		
<212>		
<213>	Homo sapiens	
<400>	89	
ccacct	ccaa ggtgtatca	19
<210>	90	
<211>		
<212>		
<213>	Homo sapiens	
<400>	90	
tgttat	gttg gctccttgct	20
<210>	91	
<211>	91 22	
	22 DNA	

<400> cactaaa	91 agac agaatgaatc ta	22
<210>	92	
<211>	22	
<212>	DNA	
<213>	Homo sapiens	
<400>	92	
gaagaad	ccag aatattcatc ta	22
	93	
<211>		
<212>		
<213>	Homo sapiens	
<400>	93	
tgatggg	ggag tctgaatcaa	20
<210>		
<211>		
<212>		
<213>	Homo sapiens	
<400>		
tctgctt	ttct tgataaaatc ct	22
<210>		
<211>		
<212>		
<213>	Homo sapiens	
	^-	
<400>	95	20
agcgtco	ccct cacaaataaa	20
.010-		
<210>	96	
<211>		
<212>		
<213>	Homo sapiens	
.400-		
<400>	96 gcat gaatatgcct	20
ccaage	grat gaatatgeet	20
<210>	97	
<210>	22	
<212>		
<213>	Homo sapiens	
<400>	97	
	gcaa tatggaactc ga	22
grarad	yeur eregguaete ga	~ ~

<210>	98	
<211>	23	
<212>	DNA	
<213>	Homo sapiens	
<400>	98	
	cac tggtatttga aca	23
coaage		
210	00	
<210>	99	
	20	
<212>		
<213>	Homo sapiens	
<400>	99	
	gata ctttcccaga	20
J J - L	,	
.010.	100	
	100	
<211>		
<212>		
<213>	Homo sapiens	
<400>	100	
tqqaaca	acc atgaattagt c	21
23		
-210-	101	
	101	
<211>	20	
<212>		
<213>	Homo sapiens	
<400>	101	
ggaagtt	agc actctaggga	20
<210>	102	
<211>	22	
<212>	DNA	
<213>	Homo sapiens	
<400>	102	
gcagtga	atat taactgtctg ta	22
<210>	103	
<211>	22	
<212>	DNA	
<213>	Homo sapiens	
<413>	nomo sabrens	
400	100	
<400>	103	
tgggtc	etta aagaaacaaa gt	22
<210>	104	
<211>	21	

<212> <213>	DNA Homo sapiens	
<400>		21
ccaggig	gaca ttgaatcttc c	21
<210> <211>	105 21	
<212>		
	Homo sapiens	
	105	
ccactti	ette ecateaagte a	21
<210>	106	
<211>		
<212>	DNA	
<213>	Homo sapiens	
	106	
tcagga	eget tacaattact te	22
<210>	107	
<211>	23	
<212>	DNA	
<213>	Homo sapiens	
<400>	107	
	igaa tgctatgctt aga	23
210	100	
<210> <211>	108 20	
	DNA	
	Homo sapiens	
	•	
<400>	108	
tcggta	accc tgagccaaat	20
<210>	109	
<211>	20	
<212>	DNA	
<213>	Homo sapiens	
<400>	109	
gcaaaa	gcgt ccagaaagga	20
<210>	110	
<211>	22	
<212>	DNA	
<213>	Homo sapiens	

<400> tatttg	110 cagt caagtettee aa	22
<210>	111	
<211>	21	
<212>	DNA	
	Homo sapiens	
<400>	111	
gtaata	ttgg caaaggcatc t	21
<210>	112	
<211>	22	
<212>	DNA	
<213>	Homo sapiens	
<400>	112	
taaaat	gtgc tccccaaaag ca	22
<210>	113	
<211>	20	
<212>	DNA	
	Homo sapiens	
<400>	113	
gtcctg	ccaa tgagaagaaa	20
_		
<210>	114	
<211>	21	
<212>	DNA	
<213>	Homo sapiens	
<400>	114	
	caaa cctaagaatg t	21
-99		
<210>	115	
<211>	21	
<212>	DNA	
<213>	Homo sapiens	
<400>	115	
aatqqa	aagc ttctcaaagt a	21
<210>	116	
<211>	21	
<212>	DNA	
<213>	Homo sapiens	
<400>	116	
	rage taggteetta e	21

<210> 117 <211> 22 <212> DNA <213> Homo sapiens	
<400> 117 ctaacctgaa ttatcactat ca	. 22
<pre><210> 118 <211> 21 <212> DNA <213> Homo sapiens <400> 118 gtgtataaat gcctgtatgc a</pre>	21
<210> 119 <211> 19 <212> DNA <213> Homo sapiens <400> 119 tggctgccca ggaagtatg	19
<210> 120 <211> 23 <212> DNA <213> Homo sapiens <400> 120 aaccagaata tctttatgta gga	23
<210> 121 <211> 22 <212> DNA <213> Homo sapiens <400> 121 aattcttaac agagaccaga ac	22
<210> 122 <211> 22 <212> DNA <213> Homo sapiens <400> 122 aaaactcttt ccagaatgtt gt	2
<210> 123 <211> 20	

<212>	DNA
<213>	Homo sapiens
. =	•
<400>	123
	aacg tgcaggattg
5-55	, - 3 3 33 3
<210>	124
	18
<212>	
<400>	124
	catg tggtttta
5	
<210>	125
<212>	
	Homo sapiens
-	•
<400>	125
ggctct	ttag cttcttagga c
<210>	126
<211>	20
<212>	DNA
<213>	Homo sapiens
<400>	126
gagaco	attt tcccagcatc
	127
<211>	20
<212>	DNA
<213>	Homo sapiens
<400>	127
ctgtca	ittet teetgtgete
<210>	128
<210>	21
<211>	DNA
<213>	Homo sapiens
-400-	120
<400>	128
cattgt	taag gaaagtggtg c
<210>	129
<211>	20
<211>	DNA
<212>	Homo sapiens
~~13 2	TOUC Sabtens

<400>	129	
atatgad	cgtg tctgctccac	20
<210>	130	
<211>	20	
<212>		
	Homo sapiens	
1220	110 21.F1-011-	
<400>	130	
	ccaa attacacagc	20
gggaac	ceau accaeage	
-210-	121	
	131	
<211>		
<212>		
<213>	Homo sapiens	
<400>	131	
aagctc	ttcc tttttgaaag tc	22
<210>	132	
<211>	22	
<212>	DNA	
<213>	Homo sapiens	
	-	
<400>	132	*
	aaat agaatagcct ct	22
	J J	
<210>	133	
	20	
<212>		
	Homo sapiens	
\2137	nomo sapiens	
<400>	133	
	tgag aggtettget	20
LCCCat	tgag aggictiget	20
.210.	7.2.4	
<210>	134	
<211>	- -	
<212>	DNA	·
<213>	Homo sapiens	
<400>	134	
gagaag	actt ctgaggctac	20
	135	
<211>	21	
<212>	DNA	
	Homo sapiens	
	_	
<400>	135	
	gaca gttccagtag t	21

<210><211><212><213>	136 23 DNA Homo sapiens	
<400>	136	23
catttt	agcc attcattcaa caa	
·	137	
<211>	22	
<212>	Homo sapiens	
<213>	HOMO Supreme	
<400>	137	22
atgaat	tgac actaatctct gc	
<210>	138	
<211>		
<212>	DNA	
<213>	Homo sapiens	
<400>	138	21
	cagga cagtagaagg a	21
geage		
<210>		
<211>	24 DNA	
<212>	1	
(213/	Nome Darie	
<400>	139	24
gaata	atata aattatatgg ctta	
<210	. 140	
<211:		
<212	DNA .	
<213	Homo sapiens	
<400	> 140	19
ccta	gtcttg ctagttctt	
.210	> 141	
	> 24	
<212	> DNA	
<213	> Homo sapiens	
400	> 141	2.4
<400	yaagtg gaaccaaatg atac	24
acci		
	140	
<210 <210		
< ∠ ⊥.		

<212> DNA <213> Homo sapiens	
<400> 142 acgtggcaaa gaattctctg aagtaa	26
<210> 143 <211> 22	
<212> DNA <213> Homo sapiens	
<400> 143 aagaagcaaa atgtaataag ga	22
<210> 144	
<211> 22 <212> DNA	
<213> Homo sapiens	
<400> 144 catttaaagc acatacatct tg	22
<210> 145	
<211> 21 <212> DNA	
<212> DNA <213> Homo sapiens	
<400> 145	21
tctagaggca aagaatcata c	
<210> 146	
<211> 22	
<212> DNA <213> Homo sapiens	
	22
<400> 146 caagattatt cctttcatta gc	22
<210> 147	
<211> 22 <212> DNA	
<212> DNA <213> Homo sapiens	
<400> 147	22
aaccaaaaca caaatctaag ag	
<210> 148	
<211> 23 <212> DNA	
<213> Homo sapiens	

<400>	148	· ·	
gtcattt	tta tatgctgctt	tac	23
_	_		
<210>	149		
<211>	21		
<212>	DNA		
<213>	Homo sapiens		
<400>	149		
ggtttta	atat ggagacacag	q	21
<210>	150		
<211>	23		
<212>	DNA		
<213>	Homo sapiens		
<400>	150		
	caa tttcaacaca	age	23
		· J -	
010	151		
<210>	151		
<211>	20		
<212>	DNA		
<213>	Homo sapiens		
<400>	151		
	gttt tggaggtagc		20
uccucus	yeer eggaggeage		
	4		
<210>	152		
<211>	21		
<212>	DNA		
<213>	Homo sapiens		
	_		
<400>	152		
	cct gattetteta	a	21
cegacei	sect gattettea	α ·	21
<210>	153		
<211>	22		
<212>	DNA		
<213>	Homo sapiens		
<400>	153		
		at	22
accatg	agc aaatgagggt		46
<210>	154		
<211>	22		
<212>	DNA		
	Homo sapiens		
	Dabtoiin		
-100-	154		
<400>	154		22
gctttt	gtct gttttcctcc	aa	22

<210>	155	
<211>	19	
<212>	DNA	
	Homo sapiens	
72137	none supreme	
<400>	155	
aaccaca	accc ttaagatga	19
<210>	156	
	20	
<212>		
<213>	Homo sapiens	
400.	150	
<400>	156	•
gcataag	ytag tggattttgc	20
<210>	157	
<211>	31	
<212>		
	Homo sapiens	
72137	nome suprems	
-1005	157	
		31
gggcccg	ggat ccatggcaat gcagatgcag c	3 1
<210>	158	
<211>	43	
<212>	DNA	
	Homo sapiens	
<400>	158	
		43
gggcccc	caat ggatatcatt cagtetttgg cateteecae tee	43
	159	
<211>	20	
<212>	DNA	
<213>	Homo sapiens	
<400>	159	
	gcat ggcgctgagg	20
040343	53-50-53-55	_
-210-	160	
<210>	160	
<211>	20	
	DNA	
<213>	Homo sapiens	
<400>	160	
ccgggc	cttg tctgtccact	20
<210>	161	
<211>	20	

<212>	DNA	
	Homo sapiens	
	-	
<400>	161	
atctace	ccca ttgaccatgg	20
J		
<210>	162	
<211>	20	
<212>		
	Homo sapiens	
<400>	162	
	cctg agtactgctg	20
<210>	163	
<211>		
<212>		
	Homo sapiens	
(213)	Homo Sapiens	
<400>	163	
	agga agaagacctg	20
cgcagg	ayaa ayaayacccy	2.0
<210>	164	
<211>		
<212>		
(213)	Homo sapiens	
<400>	164	
		20
cccgcc	agog coaggggact	2
<210>	165	
<211>	20	
<212>		
<213>	Homo sapiens	
400	105	
<400>	165	2.0
agcacag	ggcc tgctgcacct	20
-210:	166	
<210>	166	
<211>	20	
<212>	DNA	
<213>	Homo sapiens	
<400>	166	
gaaaag	ggga agtggggcag	20
.010	1.77	
<210>	167	
<211>	32	
<212>	DNA	
<213>	Homo sapiens	

<400> agcccag	167 ggcc ccaacacagc cccatggcct ct	32
<210>	168	
<211>	32	
<212>	DNA	
<213>	Homo sapiens	
<400>	168	
cttagga	agag ttttattcat tcattgatcc ag	32
<210>	169	
<211>	21	
<212>	DNA	
<213>	Homo sapiens	
<400>	169	
	acaa tgactgggct c	21
_		
<210>	170	
<211>	20	
<212>		
<213>		
<400>	170	
	cttc tgcacacagt	20
3 3		
<210>	171	
<211>	17	
<212>		
<213>		
<400>	171	17
acacga	cago gatactt	1,
212	150	
<210>	172	
<211> <212>	17 DNA	
<213>	Homo sapiens	
12137	nomo bapteno	
<400>	172	
acatga	cagt gatactt	17
<210>	173	
<211>	17	
<212>	DNA	
<213>	Homo sapiens	
<400>	173	
agtatt	tcat tggtacc	17

<210>	174
<211>	17
<212>	DNA
<213>	Homo sapiens
\ 4132	TONG Baptens
-100-	174
<400>	
agtatt	tcac tggtacc
<210>	175 .
<211>	17
	DNA
	Homo sapiens
-2.2.7	TOWN DUPTOND
<400>	175
calttg	ctcc gttttca
<210>	176
<211>	17
	DNA
<213>	Homo sapiens
<400>	176
	ctct gttttca
	, , , , , , , , , , , , , , , , , , , ,
-21A-	177
<210>	177
<211>	17
	DNA .
<213>	Homo sapiens
	•
<400>	177
	aaga agccagc
	J J J-
<210>	178
<211>	17
<212>	DNA
<213>	Homo sapiens
<400>	178
ttttta	aagg agccagc
<210>	179
<211>	17
<212>	DNA
<213>	Homo sapiens
<400>	179
gcgtcc	agaa aggagag
<210>	180

<211> 17

<212>	Homo sapiens
<400>	180
	agag aggagag
3 3	3 3 33 3
-210-	101
<210> <211>	181 17
<212>	
	Homo sapiens
<400>	181
aagtga	ctct tctgccc
<210>	182
<211>	17
<212>	
	Homo sapiens
	•
<400>	182
aagtga	ctcc tctgccc
<210>	183
<211>	
<211>	
	Homo sapiens
	•
<400>	183
tgtgcc	caga gtccagc
<210>	184
<211>	17
<212>	
<213>	
<400>	184
tgtgcc	cagg gtccagc
<210>	185
<211>	17
<212>	DNA
<213>	Homo sapiens
	_
<400>	185
ggaata	agca gaaactg
<210>	186
<211>	17
<212>	DNA
<213>	Homo sapiens

<400> ggaata	186 agcg gaaactg	17
<210>	187	
<211>	17	
<212>	DNA	
<213>	Homo sapiens	
<400>	187	
aaaaga	catg acagcga	17
<210>	188	
<211>	17	
	DNA	
	Homo sapiens	
72137	nomo baptono	
<400>	188	17
aaaaya	cata acagoga	17
<210>	189	
<211>	17	
<212>	DNA	
<213>	Homo sapiens	
<400>	189	
aagaag	ccag ctcaagc	17
<210>	190	
<211>	17	
<212>	DNA	
<213>	Homo sapiens	
<400>	190	
aagaag	ccaa ctcaagc	17
<210>	191	
<211>	17	
<212>	DNA	
<213>	Homo sapiens	
<400>	191	
	agtg atacttt	17
caegae		1,
-210-	102	
<210>	192	
<211>	17	
<212>	DNA	
<213>	Homo sapiens	
<400>	192	_
catgac	agta atacttt	17

<210>	193	
<211>	17	
<212>		
	Homo sapiens	
<400>	193	
	attg gcattga	1
caggac	aceg geacega	
<210>	194	
<211>		
<212>		
<213>	Homo sapiens	
<400>	194	
	catgt ggcattga	. 1
Layyat	lacyc gycaecga	
<210>	195	
<211>		
<212>		
	Homo sapiens	
~413 7	nomo saprens	
<400>	195	
	gattt gctacatt	1
	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
<210>	196	
<211>		
<212>		
	Homo sapiens	
-3207		
<400>	196	
	gatgt gctacatt	1
	, <u>,</u> , , , , , , , , , , , , , , , , ,	
<210>	197	
<211>	18	
<212>	DNA	
	Homo sapiens	
	-	
<400>	197	
ggctt	ctctg attttggt	1
	·	
<210>		
<211>		
<212>		
<213>		
<400>	198	
ggctt	ctcgg attttggt	1
<210>	199	

<211> 18

<212> DNA <213> Hor	A mo sapiens	
<400> 199	9	18
ttttgaata	t tgtactgg	
<210> 20 <211> 18		
<211> 18 <212> DN		
<213> Ho	omo sapiens	
<400> 20		18
ttttgaatg	gt tgtactgg	
<210> 20		
<211> 18		
<212> DN		
<213> Ho	omo sapiens	
<400> 20	01	18
	ct tggaagac	
<210> 2	02	
<211> 1		
	NA	
	omo sapiens	
<400> 2	02	18
	tt tggaagac	
<210> 2	203	
	18	
	ONA	
<213> F	Homo sapiens	
	203	18
ccatttgt	ttc atgtaatc	
<210>	204	
	18	
	DNA	
<213>	Homo sapiens	
	204	18
ccatttg	rtcc atgtaatc	
<210>	205	
<211>	18	
<212>	DNA	
<213>	Homo sapiens	

<400> tagctt	205 ggtt ttctaaac	18
<210>	206	
<211>		
<212>		
	Homo sapiens	
10201		
<400>	206	
	ggct ttctaaac	18
•	-	
<210>	207	
<211>	18	
<212>	AND	
<213>	Homo sapiens	
<400>	207	
attgaa	acaa cagaatca	18
<210>	208	
<211>		
<211>		
	Homo sapiens	
(213)	nomo sapiens	
<400>	208	
	acga cagaatca	18
•		
<210>	209	
<211>	18	
<212>		
<213>	Homo sapiens	
400		
<400>	209	18
Lyaaaa	tgtg atttagtt	10
<210>	210	
<211>	18	
<212>		
	Homo sapiens	
<400>	210	
	tgcg atttagtt	18
-		
<210>	211	
<211>		
<212>		
<213>	Homo sapiens	
<400>		٦.
ttccat	ggcc ttcctaat	18

<210>	212			
<211>	18			-
<212>	DNA			
	Homo sapiens			
(21)/	nomo suprems			
<400>	212			
	ggtc ttcctaat			•
LLCCat	ggcc ccccaac			
010	012			
	213		•	
<211>	18			
<212>	DNA			
<213>	Homo sapiens			
<400>	213			
	ggcg tatacagg			
	33-3			
		•		
<210>	214			
	18			
<212>				
<213>	Homo sapiens			
<400>	214			
cttgaa	ggtg tatacagg			
<210>	215			
<211>	19			
<212>				
<213>	Homo sapiens			
	0.1.5			
<400>	215			
atggcc	tcta ccagatggc			
<210>	216			
<211>	19			
<212>	DNA			
<213>	Homo sapiens			
	•			
<400>	216			
	ctctc ccagatggc			
~~9900	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	•		
-210-	217			
<210>				
<211>				
<212>				
<213>	Homo sapiens			•
<400>	217			
	ctctg ccagatggc			
33	5 5 55			
<210>	218			
<211>	エ フ			

<212>	DNA	
<213>	Homo sapiens	
	-	
<400>	218	
atggcc	tctt ccagatggc	
<210>	219	
	19	
<212>		
	Homo sapiens	
	•	
<400>	219	
	gctt tgaaaaagg	
	,55	
<210>	220	
	19	
<212>		
	Homo sapiens	
\213/	nomo bapieno	
<400>	220	
	gctt tgcaaaagg	
cagacg	geer tycaaaayy	
<210>	221	
<211>		
<212>		
	Homo sapiens	
(213)	HOMO Sapiens	
<400>	221	
	gctt tggaaaagg	
cagacg	geee eggaaaagg	
<210>	222	
	19	
<211>		
	Homo sapiens	
~~1J <i>></i>	nomo saprens	
<400>	222	
	gctt tgtaaaagg	
Lugary	geet tytaaaayy	
<210>	223	
<211>	19	
<211>	DNA	
<212>	Homo sapiens	
~ 213>	HOUND SAPIEUS	
-100-	222	
<400>	223	
gateda	aaca ggccccttt	
-210	224	
<210>	224	
<211>	19	
<212>	DNA	
<213>	Homo sapiens	

<400>	224	19
gatccaa	acca ggccccttt	17
<210>	225	
<211>	19	
<212>		
<213>	Homo sapiens	
<400>	225	19
gatcca	agca ggccccttt	
.010.	226	
<210>	226 19	
<211>		
	DNA	
<213>	Homo sapiens	
.400-	226	
<400>		19
gattea	atca ggccccttt	
<210>	227	
<211>	19	
<212>		
<213>	Homo sapiens	
<400>	227	
		19
cccigc	aaaa actggatca	
<210>	228	
<211>	19	
<212>		
<213>		
12137	nome supreme	
<400>	228	
	aaac actggatca	19
<210>	229	
<211>	19	
<212>	DNA	
<213>	Homo sapiens	
10207	nome papacine	
<400>	229	
	aaag actggatca	19
	555	+-
<210>	230	
<211>	19	
<212>	DNA	
<213>		
<400>	230	
	aaat actggatca	19
		4.

<210>	231		
<211>	28		
<212>	DNA		
	Homo sapiens		
12107	nome papaone		
<400>	231		
	gga tccccacttt	teatetta	28
ccatget	.gga tttttattt	teeteetg	20
<210>	232		
<211>	28		
<212>	DNA		
	Homo sapiens		
<400>	232		
		ant manat	28
ggrgged	tgc ccttccaatg	gatecact	20
<210>	233		
<211>	30		
<212>	DNA		
	Homo sapiens		
12107	nomo ouprons		
-100-	222		
<400>	233		٦.
aattcat	ggg actgactttc	tgetettgte	30
	·		
<210>	234		
<211>	26		
<212>			
	Homo sapiens		
(413/	nomo sapiens		
400	224		
	234		
tccaggt	ccc agcccaaccc	ttgtcc	26
<210>	235		
<211>	30		
<212>			
	Homo sapiens		
72137	nome ouplens		
. 1 0 0 .	225		
<400>	235		٠.
gtcctct	gac tgctcttttc	acccatctac	30
<210>	236		
<211>	26		
<212>	DNA		
<213>			
	TOWN DUPTONS		
.400:	236		
<400>			2-
gggata	cggc caggcattga	ageece	26
<210>	237		
J2115	28		

<212>	DNA Homo sapiens		
	2220 201240110		
	237		
cttgtg	ecct gactttcaac	tctgtctc	28
<210>	238		
<211>	27		
<212>			
<213>	Homo sapiens		
<400>	238		
tgggcaa	acca gccctgtcgt	ctctcca	27
-210-	220		
<210> <211>	239		
<212>			
	Homo sapiens		
<400>	239		
ccaggc	ctct gattcctcac	tgattgctc	29
<210>	240		
<211>			
<212>			
<213>	Homo sapiens		
400	0.4.0		
<400>	240	aggata	27
gccactg	gaca accaccetta	accette	٠,
<210>	241		
<211>	27		
	DNA		
<213>	Homo sapiens		
<400>	241		
	ctt gggcctgtgt	tatctcc	27
,	333 3 3		
<210>	242		
<211>	28		
<212>	DNA		
<213>	Homo sapiens		
<400>	242		
	gtg cagggtggca	agtggctc	28
<210>	243		
<211>	30		
<212>	DNA		
<213>	Homo sapiens		

<400> gtaggad	243 cctg atttccttac	tgcctcttgc	3	30
<210><211><211>	244 29 DNA			
	Homo sapiens			
<400>	244 gcac cottggtoto	staceassas		29
acaacce	cac cerrageere	cccaccyc	•	ر
<210>	245			
<211>	30			
<212>				
<213>	Homo sapiens			
<400>	245			
cactttt	atc acctttcctt	gcctctttcc	5	30
<210>	246			
<211>	30			
<212>	DNA			
<213>	Homo sapiens			
<400>	246		\	
aacttt	ccac ttgataagag	gtcccaagac	3	30
<210>	247			
<211>	29			
<212>	DNA			
<213>				
<400>	247			
acttact	ttet ceceeteete	tgttgctgc	•	29
<210>	248			
<211>	31			
<212>	DNA			
<213>	Homo sapiens			
<400>	248	2245277		2 1
acygaai	teet atggetttee	aacccaggaa ç	-	31
<210>	249			
<211>	29			
<212>	DNA			
<213>	Homo sapiens			
<400>	249			
catctc	teet eestgettet	gtctcctac		29

<210>	250	
<211>	30	
<212>		
	Homo sapiens	
72137	nome suprems	
<400>	250	
		2.0
ctgacg	caca cctattgcaa gcaagggttc	30
<210>	251	
<211>	19	
<212>	DNA	
<213>	Homo sapiens	
<400>	251	
		10
gaageg	tctc atgctggat	19
<210>	252	
<211>	20	
<212>	DNA	
<213>	Homo sapiens	
	-	
<400>	252	
	tgta gatgggtgaa	20
ggggac	tyta gatyggtgaa	20
<210>		
<211>	19	
<212>	DNA	
<213>	Homo sapiens	
	-	
<400>	253	
	gacc tatggaaac	19
CCCCCC	gade datagadad	
010	254	
	254	
<211>	19	
	DNA	
<213>	Homo sapiens	
<400>	254	
ttttca	gatc tatggaaac	19
<210>	255	
<211>	18	
<212>		
<213>	Homo sapiens	
	255	
cccttg	ccgt cccaagca	18
<210>	256	
<211>		

<212>	DNA
	Homo sapiens
	-
<400>	256
cccttg	ccat cccaagca
<210>	
<211>	
<212>	
<213>	Homo sapiens
<400>	
ctgtcc	ccgg acgatatt
<210>	
<211>	18
<212>	
<213>	Homo sapiens
4.0.0	0.50
	258
ctgtcc	ccag acgatatt
-210-	250
<210>	
<211>	
<212>	
<213>	Homo sapiens
-400	250
<400>	
geteee	cccg tggcccct
<210>	260
<210> <211>	
<211> <212>	
~~13 >	Homo sapiens
<400>	260
	cgcg tggcccct
geteet	cycy cygocodt
<210>	261
<211>	18
<212>	DNA
<213>	Homo sapiens
<400>	261
	cgac atagtgtg
	55-5-5
<210>	262
<211>	18
<212>	DNA
<213>	Homo sapiens

<400> 262 acttttcggc atagtgtg										
<210> 263 <211> 5711 <212> DNA <213> Homo sapiens										
<220> <221> CDS <222> (120)(5711) <223> omil sequences										
<400> 263 agctcgctga gacttcctgg accccgcacc aggctgtggg gtttctcaga taactgggcc	60									
cctgcgctca ggaggccttc accctctgct ctgggtaaag ttcattggaa cagaaagaa	119									
atg gat tta tct gct ctt cgc gtt gaa gaa gta caa aat gtc att aat Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn 1 5 10 15	167									
gct atg cag aaa atc tta gag tgt ccc atc tgt ctg gag ttg atc aag Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys 20 25 30	215									
gaa cct gtc tcc aca aag tgt gac cac ata ttt tgc aaa ttt tgc atg Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met 35 40 45	263									
ctg aaa ctt ctc aac cag aag aaa ggg cct tca cag tgt cct tta tgt Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys 50 55 60	311									
aag aat gat ata acc aaa agg agc cta caa gaa agt acg aga ttt agt Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser 65 70 75 80	359									
caa ctt gtt gaa gag cta ttg aaa atc att tgt gct ttt cag ctt gac Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp 85 90 95	407									
aca ggt ttg gag tat gca aac agc tat aat ttt gca aaa aag gaa aat Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn 100 105 110	455									
aac tot oot gaa cat ota aaa gat gaa gtt tot ato ato caa agt atg Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met 115 120 125	503									
ggc tac aga aac cgt gcc aaa aga ctt cta cag agt gaa ccc gaa aat Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn 130 135 140	551									
cct tcc ttg cag gaa acc agt ctc agt gtc caa ctc tct aac ctt gga Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly	599									

145	150	155	160
		ata caa cct caa aag Ile Gln Pro Gln Lys 175	
		tct gaa gat acc gtt Ser Glu Asp Thr Val 190	
		gaa ttg tta caa atc Glu Leu Leu Gln Ile 205	
		gat tct gca aaa aag Asp Ser Ala Lys Lys 220	
		aat act gaa cat cat Asn Thr Glu His His 235	
		aag cgt gca gct gag Lys Arg Ala Ala Glu 255	
		tca aac ttg cat gtg Ser Asn Leu His Val 270	
		tta cag cat gag aac Leu Gln His Glu Asn 285	
•	~ 5 5	gta gaa aag gct gaa Val Glu Lys Ala Glu 300	
-		agg agc caa cat aac Arg Ser Gln His Asn 315	•
	=	agg cgg act ccc agc Arg Arg Thr Pro Ser 335	
		ctg tgt gag aga aaa Leu Cys Glu Arg Lys 350	-
		aat cct aga gat act Asn Pro Arg Asp Thr 365	-
		att cag aaa gtt aat Ile Gln Lys Val Asn 380	

tgg Trp 385	ttt Phe	tcc Ser	aga Arg	agt Ser	gat Asp 390	gaa Glu	ctg Leu	tta Leu	ggt Gly	tct Ser 395	gat Asp	gac Asp	tca Ser	cat His	gat Asp 400	1319
ggg Gly	gag Glu	tct Ser	gaa Glu	tca Ser 405	aat Asn	gcc Ala	aaa Lys	gta Val	gct Ala 410	gat Asp	gta Val	ttg Leu	gac Asp	gtt Val 415	cta Leu	1367
aat Asn	gag Glu	gta Val	gat Asp 420	gaa Glu	tat Tyr	tct Ser	ggt Gly	tct Ser 425	tca Ser	gag Glu	aaa Lys	ata Ile	gac Asp 430	tta Leu	ctg Leu	1415
gcc Ala	agt Ser	gat Asp 435	cct Pro	cat His	gag Glu	gct Ala	tta Leu 440	ata Ile	tgt Cys	aaa Lys	agt Ser	gaa Glu 445	aga Arg	gtt Val	cac His	1463
tcc Ser	aaa Lys 450	tca Ser	gta Val	gag Glu	agt Ser	aat Asn 455	att Ile	gaa Glu	gac Asp	aaa Lys	ata Ile 460	ttt Phe	ggg ggg	aaa Lys	acc Thr	1511
tat Tyr 465	cgg Arg	aag Lys	aag Lys	gca Ala	agc Ser 470	ctc Leu	ccc Pro	aac Asn	tta Leu	agc Ser 475	cat His	gta Val	act Thr	gaa Glu	aat Asn 480	1559
cta Leu	att Ile	ata Ile	gga Gly	gca Ala 485	ttt Phe	gtt Val	act Thr	gag Glu	cca Pro 490	cag Gln	ata Ile	ata Ile	caa Gln	gag Glu 495	cgt Arg	1607
ccc Pro	ctc Leu	aca Thr	aat Asn 500	aaa Lys	tta Leu	aag Lys	cgt Arg	aaa Lys 505	agg Arg	aga Arg	cct Pro	aca Thr	tca Ser 510	ggc	ctt Leu	1655
His	Pro	Glu 515	Asp	Phe	atc Ile	Lys	Lуs 520	Ala	Asp	Leu	Ala	Val 525	Gln	Lys	Thr	1703
Pro	Glu 530	Met	Ile	Asn	cag Gln	Gly 535	Thr	Asn	Gln	Thr	Glu 540	Gln	Asn	Gly	Gln	1751
Val 545	Met	Asn	Ile	Thr	aat Asn 550	Ser	Gly	His	Glu	Asn 555	Lys	Thr	Lys	Gly	560	1799
Ser	Ile	Gln	Asn	Glu 565	Lys	Asn	Pro	Asn	570	Ile	Glu	Ser	Leu	575		1847
Glu	Ser	Ala	Phe 580	Lys	Thr	Lys	Ala	. Glu 585	Prc) Ile	Ser	Ser	590	Ile	agc Ser	1895
aat Asn	atg Met	gaa Glu 595	Leu	gaa Glu	tta Leu	aat Asn	ato Ile 600	His	aat Asn	tca Ser	aaa Lys	gca Ala 605	Pro	aaa Lys	aag Lys	1943

	agg Arg 610	_			_												1991
	gta Val	_	_	_			_				_		_	•			2039
	gat Asp																2087
	atg Met		_	_													2135
	cct Pro																2183
	aaa Lys 690																2231
	cct Pro																2279
	gtc Val			-			_	_	_		_				_		2327
	gtt Val							-								4	2375
	gga Gly																2423
	tca Ser 770																2471
	ı ctg ı Leu i																2519
	gtg Val																2567
	tgt Cys																2615
tt	g gga	cat	gaa	gtt	aac	cac	agt	cgg	gaa	aca	agc	ata	gaa	atg	gaa		2663

Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu 835 840 845	
gaa agt gaa ctt gat gct cag tat ttg cag aat aca ttc aag gtt tca Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser 850 855 860	2711
aag cgc cag tca ttt gct ctg ttt tca aat cca gga aat gca gaa gag Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu 865 870 875 880	2759
gaa tgt gca aca ttc tct gcc cac tct ggg tcc tta aag aaa caa agt Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser 885 890 895	2807
cca aaa gtc act ttt gaa tgt gaa caa aag gaa gaa aat caa gga aag Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys 900 905 910	2855
aat gag tot aat atc aag oct gta cag aca gtt aat atc act gca ggc Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly 915 920 925	2903
ttt cct gtg gtt ggt cag aaa gat aag cca gtt gat aat gcc aaa tgt Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys 930 935 940	2951
agt atc aaa gga ggc tct agg ttt tgt cta tca tct cag ttc aga ggc Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly 945 950 955 960	2999
aac gaa act gga ctc att act cca aat aaa cat gga ctt tta caa aac Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn 965 970 975	3047
cca tat cgt ata cca cca ctt ttt ccc atc aag tca ttt gtt aaa act Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr 980 985 990	3095
aaa tgt aag aaa aat ctg cta gag gaa aac ttt gag gaa cat tca atg Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met 995 1000 1005	3143
tca cct gaa aga gaa atg gga aat gag aac att cca agt aca gtg Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val 1010 1015 1020	3188
agc aca att agc cgt aat aac att aga gaa aat gtt ttt aaa gga Ser Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Gly 1025 1030 1035	3233
gcc agc tca agc aat att aat gaa gta ggt tcc agt act aat gaa Ala Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu 1040 1045 1050	3278
gtg ggc tcc agt att aat gaa ata ggt tcc agt gat gaa aac att Val Gly Ser Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile	3323

	1055					1060					1065			
	_	_			_	aac Asn 1075	_					_	_	3368
						caa Gln 1090								3413
						cat His 1105								3458
-	_	_	_	_		gtt Val 1120			_				_	3503
		_			_	cag Gln 1135		_		_	_	_		3548
						cct Pro 1150								3593
						ttt Phe 1165								3638
	_	_		-		agc Ser 1180	_	_	_			_		3683
_	cct Pro 1190					cat His 1195								3728
_	999 Gly 1205	-	_			gag Glu 1210			-				_	3773
						tgc Cys 1225								3818
-						cag Gln 1240								3863
		_	_		_	aac Asn 1255							_	3908

aag aat agc tta aat gac tgc agt aac cag gta ata ttg gca aag 3953 Lys Asn Ser Leu Asn Asp Cys Ser Asn Gln Val Ile Leu Ala Lys 1265 1270 1275

	tct Ser 1280				Ser		aaa Lys 1290			3998
	ttg Leu 1295				Ser		gac Asp 1305			4043
	aca Thr 1310						tct Ser 1320			4088
	agg Arg 1325						ctg Leu 1335			4133
	ttg Leu 1340									4178
	aat Asn 1355						tta Leu 1365	gaa Glu	_	4223
	tct Ser 1370						gaa Glu 1380	-		4268
_	cta Leu 1385						cag Gln 1395	agg Arg		4313
_	atg Met 1400						gaa Glu 1410	-	_	4358
	gaa Glu 1415			cag Gln 1420			cct Pro 1425	aac Asn		4403
	cct Pro 1430				Ser					4448
	cca Pro 1445							tca Ser	_	4493
	agt Ser 1460									4538
	gac Asp 1475									4583

						agg Arg 1495									4628
						atg Met 1510									4673
aat Asn	aga Arg 1520	aac Asn	tac Tyr	cca Pro	tct Ser	caa Gln 1525	gag Glu	gag Glu	ctc Leu	att Ile	aag Lys 1530	gtt Val	gtt Val	gat Asp	4718
	gag Glu 1535					gaa Glu 1540									4763
_	aca Thr 1550					agg Arg 1555									4808
_	gaa Glu 1565					ctc Leu 1570									4853
	tct Ser 1580	gaa Glu	gac Asp	aga Arg	gcc Ala	cca Pro 1585	gag Glu	tca Ser	gct Ala	cgt Arg	gtt Val 1590	ggc Gly	aac Asn	ata Ile	4898
	tct Ser 1595					ttg Leu 1600									4943
_	tct Ser 1610					gct Ala 1615									4988
	tat Tyr 1625					gaa Glu 1630									5033
	aca Thr 1640					agg Arg 1645									5078
	tct Ser 1655					gaa Glu 1660									5123
						act Thr 1675							gaa Glu		5168
	act Thr 1685					aaa Lys 1690						Val			5213
cgg	aca	ctg	aaa	tat	ttt	cta	gga	att	gcg	gga	gga	aaa	tgg	gta	5258

Arg	Thr 1700	Leu	Lys	Tyr	Phe	Leu 1705	Gly	Ile	Ala	Gly	Gly 1710	Lys	Trp	Val	
	agc Ser 1715	tat Tyr	ttc Phe	tgg Trp	gtg Val	acc Thr 1720	cag Gln	tct Ser	att Ile	aaa Lys	gaa Glu 1725	aga Arg	aaa Lys	atg Met	5303
_	aat Asn 1730			_		gaa Glu 1735	_	_		_		_			5348
_	aac Asn 1745					aag Lys 1750									5393
	atc Ile 1760					gaa Glu 1765									5438
	atg Met 1775			_		ctg Leu 1780	_		_	_	-	_	_		5483
_	tct Ser 1790					ctt Leu 1795									5528
_	cac His 1805				_	gtg Val 1810	_		_	_	tgg Trp 1815		gag Glu	_	5573
	ggc Gly 1820					999 Gly 1825									5618
	cga Arg 1835					gac Asp 1840									5663
	ctg Leu 1850					ata Ile 1855							cac His	tac Tyr	5708
tga															5711

<210> 264

<211> 1863

<212> PRT

<213> Homo sapiens

<400> 264

Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn 1 5 10 15

Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys 20 25 30

Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys 55 Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn 105 110 Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn 135 Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly 155 145 150 Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr 170 Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr 200 Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala 215 Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg 250 His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe 290 300 295 Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg 305 Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr 330

- Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu
 340 345 350
- Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu 355 360 365
- Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu 370 375 380
- Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp 385 390 395 400
- Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu
 405
 410
 415
- Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu 420 425 430
- Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His
 435 440 445
- Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr 450 455 460
- Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn 465 470 475 480
- Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg
 485 490 495
- Pro Leu Thr Asn Lys Leu Lys Arg Lys Arg Pro Thr Ser Gly Leu
 500 505 510
- His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr 515 520 525
- Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln 530 540
- Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp 545 550 555 560
- Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys 565 570 575
- Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser 580 585 590
- Asn Met Glu Leu Glu Leu Asn Ile His Asn Ser Lys Ala Pro Lys Lys 595 600 605
- Asn Arg Leu Arg Arg Lys Ser Ser Thr Arg His Ile His Ala Leu Glu 610 620
- Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln 625 630 635 640

Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Lys Tyr Asn 650 645 Gln Met Pro Val Arg His Ser Arg Asn Leu Gln Leu Met Glu Gly Lys 665 Glu Pro Ala Thr Gly Ala Lys Lys Ser Asn Lys Pro Asn Glu Gln Thr 680 Ser Lys Arg His Asp Ser Asp Thr Phe Pro Glu Leu Lys Leu Thr Asn 695 Ala Pro Gly Ser Phe Thr Lys Cys Ser Asn Thr Ser Glu Leu Lys Glu Phe Val Asn Pro Ser Leu Pro Arg Glu Glu Lys Glu Glu Lys Leu Glu 730 Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser 775 Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys 795 785 Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His 810 Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro 825 Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu 840 Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser 855 Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu 865 Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser 890 Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys 900 Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly 920 Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys

935

940

- Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly 945 950 955 960
- Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn 965 970 975
- Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr 980 985 990
- Lys Cys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met 995 1000 1005
- Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val 1010 1015 1020
- Ser Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Gly 1025 1030 1035
- Ala Ser Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu
 1040 1045 1050
- Val Gly Ser Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile 1055 1060 1065
- Gln Ala Glu Leu Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met 1070 1075 1080
- Leu Arg Leu Gly Val Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu 1085 1090 1095
- Pro Gly Ser Asn Cys Lys His Pro Glu Ile Lys Lys Gln Glu Tyr 1100 1105 1110
- Glu Glu Val Val Gln Thr Val Asn Thr Asp Phe Ser Pro Tyr Leu 1115 1120 1125
- Ile Ser Asp Asn Leu Glu Gln Pro Met Gly Ser Ser His Ala Ser 1130 1140
- Gln Val Cys Ser'Glu Thr Pro Asp Asp Leu Leu Asp Asp Gly Glu 1145 1150 1155
- Ile Lys Glu Asp Thr Ser Phe Ala Glu Asn Asp Ile Lys Glu Ser 1160 1165 1170
- Ser Ala Val Phe Ser Lys Ser Val Gln Arg Gly Glu Leu Ser Arg 1175 1180 1185
- Ser Pro Ser Pro Phe Thr His Thr His Leu Ala Gln Gly Tyr Arg 1190 1195 1200
- Arg Gly Ala Lys Lys Leu Glu Ser Ser Glu Glu Asn Leu Ser Ser 1205 1210 1215
- Glu Asp Glu Glu Leu Pro Cys Phe Gln His Leu Leu Phe Gly Lys 1220 1225 1230

Val	Asn 1235	Asn	Ile	Pro	Ser	Gln 1240	Ser	Thr	Arg	His	Ser 1245	Thr	Val	Ala
Thr	Glu 1250	Cys	Leu	Ser	Lys	Asn 1255		Glu	Glu	Asn	Leu 1260	Leu	Ser	Leu
Lys	Asn 1265	Ser	Leu	Asn	Asp	Cys 1270	Ser	Asn	Gln	Val	Ile 1275	Leu	Ala	Lys
Ala	Ser 1280	Gln	Glu	His	His	Leu 1285	Ser	Glu	Glu	Thr	Lys 1290	Cys	Ser	Ala
Ser	Leu 1295	Phe	Ser	Ser	Gln	Cys 1300	Ser	Glu	Leu	Glu	Asp 1305	Leu	Thr	Ala
Asn	Thr 1310	Asn	Thr	Gln	Asp	Pro 1315	Phe	Leu	Ile	Gly	Ser 1320	Ser	Lys	Gln
Met	Arg 1325	His	Gln	Ser	Glu	Ser 1330	Gln	Gly	Val	Gly	Leu 1335	Ser	Asp	Lys
Glu	Leu 1340	Val	Ser	Asp	Asp	Glu 1345	Glu	Arg	Gly	Thr	Gly 1350	Leu	Glu	Glu
Asn	Asn 1355		Glu	Glu	Gln	Ser 1360	Met	Asp	Ser	Asn	Leu 1365	Gly	Glu	Ala
Ala	Ser 1370	Gly	Cys	Glu	Ser	Glu 1375	Thr	Ser	Val	Ser	Glu 1380	Asp	Cys	Ser
Gly	Leu 1385	Ser	Ser	Gln	Ser	Asp 1390	Ile	Leu	Thr	Thr	Gln 1395		Arg	Asp
Thr	Met 1400	Gln	His	Asn	Leu	Ile 1405	Lys	Leu	Gln	Gln	Glu 1410	Met	Ala	Glu
Leu	Glu 1415	Ala	Val	Leu		Gln 1420	His	Gly	Ser	Gln	Pro 1425	Ser	Asn	Ser
Tyr	Pro 1430	Ser	Ile	Ile	Ser	Asp 1435	Ser	Ser	Ala	Leu	Glu 1440	Asp	Leu	Arg
Asn	Pro 1445	Glu	Gln	Ser	Thr	Ser 1450	Glu	Lys	Ala	Val	Leu 1455		Ser	Gln
Lys	Ser 1460	Ser	Glu	Tyr	Pro	Ile 1465	Ser	Gln	Asn	Pro	Glu 1470	Gly	Leu	Ser
Ala	Asp 1475	_	Phe	Glu	Val	Ser 1480	Ala	Asp	Ser	Ser	Thr 1485		Lys	Asn
Lys	Glu 1490	Pro	Gly	Val	Glu	Arg 1495	Ser	Ser	Pro	Ser	Lys 1500	Сув	Pro	Ser
Leu	Asp 1505	-	Arg	Trp	Tyr	Met 1510	His	Ser	Cys	Ser	Gly 1515		Leu	Gln

Asn Arg 1520		Tyr	Pro	Ser	Gln 1525	Glu	Glu	Leu	Ile	Lys 1530	Val	Val	Asp
Val Glu 1535		Gln	Gln	Leu	Glu 1540	Glu	Ser	Gly	Pro	His 1545	Asp	Leu	Thr
Glu Thr 1550		Tyr	Leu	Pro	Arg 1555		Asp	Leu	Glu	Gly 1560	Thr	Pro	Tyr
Leu Glu 1565		Gly	Ile	Ser	Leu 1570	Phe	Ser	Asp	Asp	Pro 1575	Glu	Ser	Asp
Pro Ser 1580		Asp	Arg	Ala	Pro 1585	Glu	Ser	Ala	Arg	Val 1590	Gly	Asn	Ile
Pro Ser 1595		Thr	Ser	Ala	Leu 1600	Lys	Val	Pro	Gln	Leu 1605	Lys	Val	Ala
Glu Ser 1610		Gln	Gly	Pro	Ala 1615	Ala	Ala	His	Thr	Thr 1620	Asp	Thr	Ala
Gly Tyr 1625		Ala	Met	Glu	Glu 1630	Ser	Val	Ser	Arg	Glu 1635	Lys	Pro	Glu
Leu Thr 1640		Ser	Thr	Glu	Arg 1645	Val	Asn	Lys	Arg	Met 1650	Ser	Met	Val
Val Ser 1655	_	Leu	Thr	Pro	Glu 1660	Glu	Phe	Met	Leu	Val 1665	Tyr	Lys	Phe
Ala Arg 1670	_	His	His	Ile	Thr 1675	Leu	Thr	Asn	Leu	Ile 1680	Thr	Glu	Glu
Thr Thr 1685		Val	Val	Met	Lys 1690	Thr	Asp	Ala	Glu	Phe 1695	Val	Cys	Glu
Arg Thr 1700		Lys	Tyr	Phe	Leu 1705	Gly	Ile	Ala	Gly	Gly 1710	Lys	Trp	Val
Val Ser 1715	_	Phe	Trp	Val	Thr 1720	Gln	Ser	Ile	Lys	Glu 1725	Arg	Lys	Met
Leu Asn 1730		His	Asp	Phe	Glu 1735	Val	Arg	Gly	Asp	Val 1740	Val	Asn	Gly
Arg Asn 1745		Gln	Gly	Pro	Lys 1750	Arg	Ala	Arg	Glu	Ser 1755	Gln	Asp	Arg
Lys Ile 1760		Arg	Gly	Leu	Glu 1765	Ile	Сув	Cys	Tyr	Gly 1770	Pro	Phe	Thr
Asn Met 1775		Thr	Asp	Gln	Leu 1780	Glu	Trp	Met	Val	Gln 1785	Leu	Сув	Gly
Ala Ser 1790		Val	Lys	Glu	Leu 1795	Ser	Ser	Phe	Thr	Leu 1800	Gly	Thr	Gly

Val His Pro Ile Val Val Gln Pro Asp Ala Trp Thr Glu Asp 1805 1810 1810	
Asn Gly Phe His Ala Ile Gly Gln Met Cys Glu Ala Pro Val Val 1820 1825 1830	
Thr Arg Glu Trp Val Leu Asp Ser Val Ala Leu Tyr Gln Cys Gln 1835 1840 1845	
Glu Leu Asp Thr Tyr Leu Ile Pro Gln Ile Pro His Ser His Tyr 1850 1855 1860	
<210> 265 <211> 5711 <212> DNA <213> Homo sapiens	
<220> <221> CDS <222> (120)(5711) <223> omi2 sequences	
<400> 265 agctcgctga gacttcctgg accccgcacc aggctgtggg gtttctcaga taactggg	jec 60
cctgcgctca ggaggccttc accctctgct ctgggtaaag ttcattggaa cagaaaga	aa 119
atg gat tta tct gct ctt cgc gtt gaa gaa gta caa aat gtc att aat Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asr 1 5 10 15	
gct atg cag aaa atc tta gag tgt ccc atc tgt ctg gag ttg atc aag Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys 20 25 30	
gaa cct gtc tcc aca aag tgt gac cac ata ttt tgc aaa ttt tgc atg Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met 35 40 45	
ctg aaa ctt ctc aac cag aag aaa ggg cct tca cag tgt cct tta tgt Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys 50 55 60	
aag aat gat ata acc aaa agg agc cta caa gaa agt acg aga ttt agt Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser 65 70 75 80	
caa ctt gtt gaa gag cta ttg aaa atc att tgt gct ttt cag ctt gad Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp 85 90 95	
aca ggt ttg gag tat gca aac agc tat aat ttt gca aaa aag gaa aat Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn 100 105 110	

			_				_	_	-				caa Gln	_	-	503
~~		_		_	_		_			_	_	_	ccc Pro	-		551
		_	_	_		_		_	-				aac Asn			599
		_		_			_	_					caa Gln	_	_	647
	_			_	_			_			_	_	acc Thr 190	_		695
													caa Gln			743
													aaa Lys			791
													cat His			839
													gct Ala			887
			_		_		~		_			_	cat His 270	-	~ -	935
	_						_	_			_		gag Glu			983
_						_	_	_		-	_	_	gct Ala	-		1031
													cat His			1079
													ccc Pro			1127
gaa	aaa	aag	gta	gat	ctg	aat	gct	gat	ccc	ctg	tgt	gag	aga	aaa	gaa	1175

Glu	Lys	Lys	Val 340	Asp	Leu	Asn	Ala	Asp 345	Pro	Leu	Cys	Glu	Arg 350	Lys	Glu	
		_	_		~		_					-	gat Asp		-	1223
_	_							_	-		_		gtt Val			1271
													tca Ser			1319
													gac Asp			1367
		_	_	-						-			gac Asp 430			1415
													aga Arg			1463
													gly ggg			1511
													act Thr			1559
													caa Gln			1607
													tca Ser 510			1655
													caa Gln			1703
													aat Asn			1751
													aaa Lys			1799
													ctc Leu			1847

	565	570	575	
	-	-	c agc agt ata agc r Ser Ser Ile Ser 590	1895
		e His Asn Ser Ly	a gca cct aaa aag s Ala Pro Lys Lys 605	1943
			t cat gcg ctt gaa e His Ala Leu Glu 0	1991
	-	_	t act gaa ttg caa s Thr Glu Leu Gln 640	2039
			a aaa aag tac aac s Lys Lys Tyr Asn 655	2087
			c atg gaa ggt aaa u Met Glu Gly Lys 670	2135
-		s Ser Asn Lys Pr	a aat gaa cag aca o Asn Glu Gln Thr 685	2183
			g aag tta aca aat u Lys Leu Thr Asn 0	2231
		_	t gaa ctt aaa gaa r Glu Leu Lys Glu 720	2279
_	_		a gag aaa cta gaa u Glu Lys Leu Glu 735	2327
	-		a gat ctc atg tta s Asp Leu Met Leu 750	2375
		r Glu Arg Ser Va	a gag agt agc agt l Glu Ser Ser Ser 765	2423
			g gaa agt atc tcg n Glu Ser Ile Ser 0	2471
			a gaa cca aat aaa r Glu Pro Asn Lys 800	2519

				•												
tgt g Cys V	_	_	_	-	_	_		_			_					2567
ggt t Gly C																2615
ttg g			-	_			_		_		_		_	_	_	2663
gaa a Glu S	_	_		_		_		_	_				-			2711
aag c Lys A 865	_	_			-	_							- 7	-		2759
gaa t Glu C																2807
cca a Pro I																2855
aat g Asn G	_				_		_	_		_				_		2903
ttt c Phe F																2951
agt a Ser I 945																2999
aac c Asn C																3047
cca t Pro T	tat Tyr	cgt Arg	ata Ile 980	cca Pro	cca Pro	ctt Leu	ttt Phe	ccc Pro 985	atc Ile	aag Lys	tca Ser	ttt Phe	gtt Val 990	aaa Lys	act Thr	3095
aaa t Lys (Gl					u H		ca atg er Met	3143
tca d Ser I		Glu					y A				le P			aca (_	3188

-	aca Thr 1025					aac Asn 1030									3	3233
	agc Ser 1040					aat Asn 1045	_	-			_			_	3	3278
	ggc Gly 1055					gaa Glu 1060									3	3323
						aac Asn 1075									3	3368
						caa Gln 1090									3	3413
	gga Gly 1100			_		cat His 1105									3	3458
						gtt Val 1120									3	3503
_	tca Ser 1130	_			_	cag Gln 1135		_		-	_		_	tct Ser	3	3548
						cct Pro 1150									3	3593
_	aag Lys 1160					ttt Phe 1165									3	3638
	gct Ala 1175					agc Ser 1180										3683
_	cct Pro 1190					cat His 1195									3	3728
						gag Glu 1210									3	3773
	_	-				tgc Cys 1225	Phe			_					3	3818
gta	aac	aat	ata	cct	tct	cag	tct	act	agg	cat	agc	acc	gtt	gct	3	3863

Val	Asn 1235	Asn	Ile	Pro	Ser	Gln 1240	Ser	Thr	Arg	His	Ser 1245	Thr	Val	Ala	
	gag Glu 1250														3908
	aat Asn 1265					-	_			_	ata Ile 1275				3953
	tct Ser 1280					ctt Leu 1285					aaa Lys 1290				3998
	ttg Leu 1295														4043
	aca Thr 1310			_	_			_							4088
	agg Arg 1325										ctg Leu 1335		_	aag Lys	4133
_	ttg Leu 1340	_		_	_	_	-	-		_		_	_	_	4178
	aat Asn 1355					agc Ser 1360		_			tta Leu 1365		gaa Glu	_	4223
	tct Ser 1370					gaa Glu 1375					gaa Glu 1380				4268
	cta Leu 1385			_	_	~					cag Gln 1395	_	~ -	_	4313
	atg Met 1400				_		_		_	_	_	-	_	_	4358
	gaa Glu 1415														4403
	cct Pro 1430														4448
	cca Pro								_	_	tta Leu			_	4493

	1445					1450					1455				
aaa Lys	agt Ser 1460	Ser	gaa Glu	tac Tyr	cct Pro	ata Ile 1465	Ser	cag Gln	aat Asn	cca Pro	gaa Glu 1470	ggc Gly	ctt Leu	tct Ser	4538
gct Ala	gac Asp 1475	Lys	ttt Phe	gag Glu	gtg Val	tct Ser 1480	gca Ala	gat Asp	agt Ser	tct Ser	acc Thr 1485	agt Ser	aaa Lys	aat Asn	4583
aaa Lys	gaa Glu 1490	Pro	gga Gly	gtg Val	gaa Glu	agg Arg 1495	tca Ser	tcc Ser	cct Pro	tct Ser	aaa Lys 1500	tgc Cys	cca Pro	tca Ser	4628
		Asp				atg Met 1510									4673
						caa Gln 1525									4718
	gag Glu 1535					gaa Glu 1540									4763
	aca Thr 1550					agg Arg 1555									4808
	gaa Glu 1565					ctc Leu 1570									4853
	tct Ser 1580					cca Pro 1585									4898
	tct Ser 1595					ttg Leu 1600									4943
	tct Ser 1610	gcc Ala	cag Gln	ggt Gly	cca Pro	gct Ala 1615	gct Ala	gct Ala	cat His	act Thr	act Thr 1620	gat Asp	act Thr	gct Ala	4988
	tat Tyr 1625	aat Asn	gca Ala	atg Met	gaa Glu	gaa Glu 1630	agt Ser	gtg Val	agc Ser	agg Arg	gag Glu 1635	aag Lys	cca Pro	gaa Glu	5033
ttg Leu	aca Thr 1640	gct Ala	tca Ser	aca Thr	gaa Glu	agg Arg 1645	gtc Val	aac Asn	aaa Lys	aga Arg	atg Met 1650	tcc Ser	atg Met	gtg Val	5078
gtg Val	tct Ser 1655	ggc Gly	ctg Leu	acc Thr	cca Pro	gaa Glu 1660	gaa Glu	ttt Phe	atg Met	ctc Leu	gtg Val 1665	tac Tyr	aag Lys	ttt Phe	5123

gcc a Ala A 1	_									-		5168
act a Thr T		_	_	_			_	_		 _	_	5213
cgg a Arg T 1												5258
gtt a Val S 1	_					_						5303
ctg a Leu A 1												5348
aga a Arg A 1												5393
aag a Lys I 1												5438
aac a Asn M 1												5483
gct t Ala S 1												5528
gtc c Val H 1					gtg Val 1810							5573
aat g Asn G 1												5618
acc c Thr A 1												5663
gag c Glu L 1						Pro						5708
tga												5711

- <211> 1863
- <212> PRT
- <213> Homo sapiens
- <400> 266
- Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn 1 5 10 15
- Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys 20 25 30
- Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met
 35 40 45
- Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys 50 55 60
- Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser 65 70 75 80
- Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp 85 90 95
- Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn 100 105 110
- Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met 115 120 125
- Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn 130 135 140
- Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly
 145 150 155 160
- Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr 165 170 175
- Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn 180 185 190
- Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr 195 200 205
- Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala 210 215 220
- Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln 225 230 235 240
- Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg 245 250 255
- His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu 260 265 270
- Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser

Ser	Leu	Leu	Leu	Thr	Lys	Asp	Arg	Met	Asn	Val	Glu	Lys	Ala	Glu	Phe
	290					295					300				

280

275

325

Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg

285

Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr

330

Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu 340 345 350

Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu 355 360 365

Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu 370 375 380

Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp 385 390 395 400

Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu 405 410 415

Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu 420 425 430

Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His
435 440 445

Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr 450 455 460

Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn 465 470 475 480

Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg 485 490 495

Pro Leu Thr Asn Lys Leu Lys Arg Lys Arg Arg Pro Thr Ser Gly Leu 500 505 510

His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr 515 520 525

Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln 530 540

Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp 545 550 555 560

Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys 565 570 575

Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser

			580					585					590		
Asn	Met	Glu 595	Leu	Glu	Leu	Asn	Ile 600	His	Asn	Ser	Lys	Ala 605	Pro	Lys	Lys
Asn	Arg	Leu	Arg	Arg	Lys	Ser	Ser	Thr	Arg	His	Ile	His	Ala	Leu	Glu

615

610

Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln 625 630 635 640

Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Lys Tyr Asn 645 650 655

Gln Met Pro Val Arg His Ser Arg Asn Leu Gln Leu Met Glu Gly Lys 660 665 670

Glu Pro Ala Thr Gly Ala Lys Lys Ser Asn Lys Pro Asn Glu Gln Thr 675 680 685

Ser Lys Arg His Asp Ser Asp Thr Phe Pro Glu Leu Lys Leu Thr Asn 690 695 700

Ala Pro Gly Ser Phe Thr Lys Cys Ser Asn Thr Ser Glu Leu Lys Glu 705 710 715 720

Phe Val Asn Pro Ser Leu Pro Arg Glu Glu Lys Glu Glu Lys Leu Glu
725 730 735

Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu 740 745 750

Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ser 755 760 765

Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser 770 775 780

Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys 785 790 795 800

Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His 805 810 815

Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro 820 825 830

Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu 835 840 845

Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser 850 855 860

Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu 865 870 875 880

Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser

885	890	895
	• • • • • • • • • • • • • • • • • • • •	030

- Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys 900 905 910
- Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly
 915 920 925
- Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys 930 935 940
- Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly 945 950 955 960
- Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn 965 970 975
- Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr 980 985 990
- Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met 995 1000 1005
- Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val 1010 1015 1020
- Ser Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Gly 1025 1030 1035
- Ala Ser Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu 1040 1045 1050
- Val Gly Ser Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile 1055 1060 1065
- Gln Ala Glu Leu Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met 1070 1075 1080
- Leu Arg Leu Gly Val Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu 1085 1090 1095
- Pro Gly Ser Asn Cys Lys His Pro Glu Ile Lys Lys Gln Glu Tyr 1100 1105 1110
- Glu Glu Val Val Gln Thr Val Asn Thr Asp Phe Ser Pro Tyr Leu 1115 1120 1125
- Ile Ser Asp Asn Leu Glu Gln Pro Met Gly Ser Ser His Ala Ser 1130 1135 1140
- Gln Val Cys Ser Glu Thr Pro Asp Asp Leu Leu Asp Asp Gly Glu 1145 1150 1155
- Ile Lys Glu Asp Thr Ser Phe Ala Glu Asn Asp Ile Lys Glu Ser 1160 1165 1170
- Ser Ala Val Phe Ser Lys Ser Val Gln Arg Gly Glu Leu Ser Arg

117	5				1180					1185			
Ser Pro 119		Pro	Phe	Thr	His 1195	Thr	His	Leu	Ala	Gln 1200	Gly	Tyr	Arg
Arg Gly 120		Lys	Lys	Leu	Glu 1210	Ser	Ser	Glu	Glu	Asn 1215	Leu	Ser	Ser
Glu Asp 122		Glu	Leu	Pro	Cys 1225	Phe	Gln	His	Leu	Leu 1230	Phe	Gly	Lys
Val Asn 123		Ile	Pro	Ser	Gln 1240	Ser	Thr	Arg	His	Ser 1245	Thr	Val	Ala
Thr Glu 125	_	Leu	Ser	Lys	Asn 1255	Thr	Glu	Glu	Asn	Leu 1260	Leu	Ser	Leu
Lys Asn 126		Leu	Asn	Asp	Cys 1270	Ser	Asn	Gln	Val	Ile 1275	Leu	Ala	Lys
Ala Ser 128		Glu	His	His	Leu 1285	Ser	Glu	Glu	Thr	Lys 1290	Cys	Ser	Ala
Ser Leu 129		Ser	Ser	Gln	Cys 1300	Ser	Glu	Leu	Glu	Asp 1305	Leu	Thr	Ala
Asn Thr		Thr	Gln	Asp	Pro 1315	Phe	Leu	Ile	Gly	Ser 1320	Ser	Lys	Gln
Met Arg		Gln	Ser	Glu	Ser 1330	Gln	Gly	Val	Gly	Leu 1335	Ser	Asp	Lys
Glu Leu 134		Ser	Asp	Asp	Glu 1345	Glu	Arg	Gly	Thr	Gly 1350	Leu	Glu	Glu
Asn Asn 135		Glu	Glu	Gln	Ser 1360	Met	Asp	Ser	Asn	Leu 1365	Gly	Glu	Ala
Ala Ser 137		Cys	Glu	Ser	Glu 1375	Thr	Ser	Val	Ser	Glu 1380	Asp	Сув	Ser
Gly Leu 138		Ser	Gln	Ser	Asp 1390	Ile	Leu	Thr	Thr	Gln 1395	Gln	Arg	Asp
Thr Met		His	Asn	Leu	Ile 1405	Lys	Leu	Gln	Gln	Glu 1410	Met	Ala	Glu
Leu Glu 141		Val	Leu	Glu	Gln 1420	His	Gly	Ser	Gln	Pro 1425	Ser	Asn	Ser
Tyr Pro 143		Ile	Ile	Ser	Asp 1435	Ser	Ser	Ala	Leu	Glu 1440	Asp	Leu	Arg
Asn Pro 144		Gln	Ser	Thr	Ser 1450	Glu	Lys	Ala	Val	Leu 1455	Thr	Ser	Gln
Lys Ser	Ser	Glu	Tyr	Pro	Ile	Ser	Gln	Asn	Pro	Glu	Gly	Leu	Ser

	1460					1465					1470			
Ala	Asp 1475	Lys	Phe	Glu	Val	Ser 1480	Ala	Asp	Ser	Ser	Thr 1485	Ser	Lys	Asn
Lys	Glu 1490	Pro	Gly	Val	Glu	Arg 1495	Ser	Ser	Pro	Ser	Lys 1500	Cys	Pro	Ser
Leu	Asp 1505	Asp	Arg	Trp	Tyr	Met 1510	His	Ser	Cys	Ser	Gly 1515	Ser	Leu	Gln
Asn	Arg 1520	Asn	Tyr	Pro	Ser	Gln 1525	Glu	Glu	Leu	Ile	Lys 1530	Val	Val	Asp
Val	Glu 1535	Glu	Gln	Gln	Leu	Glu 1540	Glu	Ser	Gly	Pro	His 1545	Asp	Leu	Thr
Glu	Thr 1550	Ser	Tyr	Leu	Pro	Arg 1555	Gln	Asp	Leu	Glu	Gly 1560	Thr	Pro	Tyr
Leu	Glu 1565	Ser	Gly	Ile	Ser	Leu 1570	Phe	Ser	Asp	Asp	Pro 1575	Glu	Ser	Asp
Pro	Ser 1580	Glu	Asp	Arg	Ala	Pro 1585	Glu	Ser	Ala	Arg	Val 1590	Gly	Asn	Ile
Pro	Ser 1595	Ser	Thr	Ser	Ala	Leu 1600	Lys	Val	Pro	Gln	Leu 1605	Lys	Val	Ala
Glu	Ser 1610	Ala	Gln	Gly	Pro	Ala 1615	Ala	Ala	His	Thr	Thr 1620	Asp	Thr	Ala
Gly	Tyr 1625	Asn	Ala	Met	Glu	Glu 1630	Ser	Val	Ser	Arg	Glu 1635	Lys	Pro	Glu
Leu	Thr 1640	Ala	Ser	Thr	Glu	Arg 1645	Val	Asn	Lys	Arg	Met 1650	Ser	Met	Val
Val	Ser 1655	Gly	Leu	Thr	Pro	Glu 1660	Glu	Phe	Met	Leu	Val 1665	Tyr	Lys	Phe
Ala	Arg 1670	Lys	His	His	Ile	Thr 1675	Leu	Thr	Asn	Leu	Ile 1680	Thr	Glu	Glu
Thr	Thr 1685	His	Val	Val	Met	Lys 1690	Thr	Asp	Ala	Glu	Phe 1695	Val	Cys	Glu
Arg	Thr 1700	Leu	Lys	Tyr	Phe	Leu 1705	Gly	Ile	Ala	Gly	Gly 1710	Lys	Trp	Val
Val	Ser 1715	Tyr	Phe	Trp	Val	Thr 1720	Gln	Ser	Ile	Lys	Glu 1725	Arg	Lys	Met
Leu	Asn 1730	Glu	His	Asp	Phe	Glu 1735	Val	Arg	Gly	Asp	Val 1740	Val	Asn	Gly
			_				*				_			

Arg Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg

1745	1750	1755
Lys Ile Phe Arg Gly Leu 1760	Glu Ile Cys Cys Tyr 1765	Gly Pro Phe Thr 1770
Asn Met Pro Thr Asp Gln 1775	Leu Glu Trp Met Val 1780	Gln Leu Cys Gly 1785
Ala Ser Val Val Lys Glu 1790	Leu Ser Ser Phe Thr 1795	Leu Gly Thr Gly 1800
Val His Pro Ile Val Val 1805	Val Gln Pro Asp Ala 1810	Trp Thr Glu Asp 1815
Asn Gly Phe His Ala Ile 1820	Gly Gln Met Cys Glu 1825	Ala Pro Val Val 1830
Thr Arg Glu Trp Val Leu 1835	Asp Ser Val Ala Leu 1840	Tyr Gln Cys Gln 1845
Glu Leu Asp Thr Tyr Leu 1850	Ile Pro Gln Ile Pro 1855	His Ser His Tyr 1860
<210> 267 <211> 5711 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (120)(5711) <223> omi3 sequences		
<400> 267 agctcgctga gacttcctgg ac	cccgcacc aggctgtggg gt	tttctcaga taactgggcc 60
cctgcgctca ggaggccttc ac	cctctgct ctgggtaaag tt	ccattggaa cagaaagaa 119
atg gat tta tct gct ctt Met Asp Leu Ser Ala Leu 1 5		
gct atg cag aaa atc tta Ala Met Gln Lys Ile Leu 20		
gaa cct gtc tcc aca aag Glu Pro Val Ser Thr Lys 35		
ctg aaa ctt ctc aac cag Leu Lys Leu Leu Asn Gln 50		ln Cys Pro Leu Cys
aag aat gat ata acc aaa Lys Asn Asp Ile Thr Lys		

65	70	75	80
	_	c att tgt gct ttt cag e Ile Cys Ala Phe Gln 90	•
		aat ttt gca aaa aag Asn Phe Ala Lys Lys 110	_
_		a gtt tct atc atc caa 1 Val Ser Ile Ile Gln 125	
		c cta cag agt gaa ccc Leu Gln Ser Glu Pro 140	_
		gtc caa ctc tct aac Val Gln Leu Ser Asn 155	
	Arg Thr Lys Glr	g cgg ata caa cct caa n Arg Ile Gln Pro Gln 170	
2		t tct tct gaa gat acc Ser Ser Glu Asp Thr 190	_
		caa gaa ttg tta caa o Gln Glu Leu Leu Gln 205	
	-	t ttg gat tct gca aaa r Leu Asp Ser Ala Lys 220	
		a aca aat act gaa cat l Thr Asn Thr Glu His 235	
-	Leu Asn Thr Thi	t gag aag cgt gca gct r Glu Lys Arg Ala Ala 250	
		t gtt tca aac ttg cat r Val Ser Asn Leu His 5 270	
		c tca tta cag cat gag r Ser Leu Gln His Glu 285	
		g aat gta gaa aag gct t Asn Val Glu Lys Ala 300	

tgt aat aaa agc aaa c Cys Asn Lys Ser Lys G 305	ag cct ggc In Pro Gly	Dea Mra	gg agc caa cat a rg Ser Gln His A 15	ac aga sn Arg 320	1079
tgg gct gga agt aag g Trp Ala Gly Ser Lys G 325	gaa aca tgt Glu Thr Cys	aat gat a Asn Asp A 330	gg cgg act ccc a rg Arg Thr Pro S	gc aca Ser Thr 335	1127
gaa aaa aag gta gat Glu Lys Lys Val Asp 3	ctg aat gct Leu Asn Ala	gat ccc c Asp Pro I 345	tg tgt gag aga a eu Cys Glu Arg l 350	aaa gaa Lys Glu	1175
tgg aat aag cag aaa Trp Asn Lys Gln Lys 355	ctg cca tgo Leu Pro Cys 360	s ser Gru F	aat cct aga gat a Asn Pro Arg Asp ' 365	act gaa Thr Glu	1223
gat gtt cct tgg ata Asp Val Pro Trp Ile 370	aca cta aat Thr Leu Ası 375	agc agc a n Ser Ser 1	att cag aaa gtt Ile Gln Lys Val 380	aat gag Asn Glu	1271
tgg ttt tcc aga agt Trp Phe Ser Arg Ser 385	gat gaa ct Asp Glu Le 390	u neu dry	tct gat gac tca Ser Asp Asp Ser 395	cat gat His Asp 400	1319
ggg gag tct gaa tca Gly Glu Ser Glu Ser 405	aat gcc aa Asn Ala Ly	a gta gct s Val Ala 410	gat gta ttg gac Asp Val Leu Asp	gtt cta Val Leu 415	1367
aat gag gta gat gaa Asn Glu Val Asp Glu 420	tat tct gg Tyr Ser Gl	t tct tca y Ser Ser 425	gag aaa ata gac Glu Lys Ile Asp 430	tta ctg Leu Leu	1415
gcc agt gat cct cat Ala Ser Asp Pro His 435	gag gct tt Glu Ala Le	eu lie cys	aaa agt gaa aga Lys Ser Glu Arg 445	gtt cac Val His	1463
tcc aaa tca gta gag Ser Lys Ser Val Glu 450	agt aat at Ser Asn II 455	tt gaa gac le Glu Asp	aaa ata ttt ggg Lys Ile Phe Gly 460	aaa acc Lys Thr	1511
tat cgg aag aag gca Tyr Arg Lys Lys Ala 465	a agc ctc c a Ser Leu P 470	cc aac tta ro Asn Leu	agc cat gta act Ser His Val Thr 475	gaa aat Glu Asn 480	1559
cta att ata gga gca Leu Ile Ile Gly Ala 489	a Phe Val 1	ct gag cca hr Glu Pro 490	GIII 110	gag cgt Glu Arg 495	1607
ccc ctc aca aat aa Pro Leu Thr Asn Ly 500	a tta aag c s Leu Lys A	gt aaa agg Arg Lys Arg 505	aga cct aca tca Arg Pro Thr Se: 51	-	1655
cat cct gag gat tt His Pro Glu Asp Ph 515	e lie ras i	aaa gca gat Lys Ala Asp 520	ttg gca gtt ca Leu Ala Val Gl 525	a aag act n Lys Thr	1703

	_	_			cag Gln					_		_				1751
					aat Asn 550	_			_							1799
		_			aaa Lys						-			_		1847
-		-			acg Thr		_	-			-	_	-		-	1895
	_	_		_	tta Leu							-			-	1943
					aag Lys											1991
	_		-	_	aat Asn 630		_				_					2039
					agc Ser											2087
					cac His											2135
					gcc Ala											2183
					agc Ser											2231
					act Thr 710											2279
	_			_	ctt Leu		_	_	_		_				_	2327
					aat Asn											2375
agt	gga	gaa	agg	gtt	ttg	caa	act	gaa	aga	tct	gta	gag	agt	agc	agt	2423

Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser 765	
att tca ttg gta cct ggt act gat tat ggc act cag gaa agt atc tcg Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser 770 780	2471
tta ctg gaa gtt agc act cta ggg aag gca aaa aca gaa cca aat aaa Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys 795 790 795	2519
tgt gtg agt cag tgt gca gca ttt gaa aac ccc aag gga cta att cat Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His 805	2567
ggt tgt tcc aaa gat aat aga aat gac aca gaa ggc ttt aag tat cca Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro 820 825	2615
ttg gga cat gaa gtt aac cac agt cgg gaa aca agc ata gaa atg gaa Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu 845	2663
gaa agt gaa ctt gat gct cag tat ttg cag aat aca ttc aag gtt tca Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser 850	2711
aag cgc cag tca ttt gct ctg ttt tca aat cca gga aat gca gaa gag Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu 875 880	2759
gaa tgt gca aca ttc tct gcc cac tct ggg tcc tta aag aaa caa agt Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser 895	2807
cca aaa gtc act ttt gaa tgt gaa caa aag gaa gaa aat caa gga aag Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys 900 905	2855
aat gag tot aat ato aag oot gta oag aca gtt aat ato act goa ggo Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly 915 920 925	2903
ttt cct gtg gtt ggt cag aaa gat aag cca gtt gat aat gcc aaa tgt Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys 930 935	2951
agt atc aaa gga ggc tct agg ttt tgt cta tca tct cag ttc aga ggc Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly 945 950 955 960	2999
aac gaa act gga ctc att act cca aat aaa cat gga ctt tta caa aac Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn 975 965	3047
cca tat cgt ata cca cca ctt ttt ccc atc aag tca ttt gtt aaa act Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr	3095

980 985 990

	aag aaa Lys Lys 995						ı His		3143
tca cct Ser Pro 1010			gga aat Gly Asi 1015				-		3188
agc aca Ser Thr 1025		_	aac att Asn Ile 1030	-	_	_		•	3233
gcc agc Ala Ser 1040			aat gaa Asn Gli 1045						3278
	tcc agt Ser Ser		-		-				3323
caa gca Gln Ala 1070			aac aga Asn Arg 1075						3368
	tta ggg Leu Gly								3413
cct gga Pro Gly 1100		_	cat cc His Pro	-		_	_		3458
gaa gaa Glu Glu 1115			gtt aar Val Ass 1120						3503
att tca Ile Ser 1130	-		cag cc Gln Pro 1135						3548
	tgt tct Cys Ser								3593
	gaa gat Glu Asp								3638
	gtt ttt Val Phe								3683
	agc cct Ser Pro								3728

										aac Asn 1215				3773
										tta Leu 1230		ggt Gly		3818
										agc Ser 1245		gtt Val	-	3863
										tta Leu 1260				3908
										ata Ile 1275		gca Ala	_	3953
										aaa Lys 1290				3998
_	_			_	_	_	-	_	_	gac Asp 1305	_		_	4043
										tct Ser 1320		aaa Lys		4088
										ctg Leu 1335		gac Asp	_	4133
										ggc Gly 1350				4178
		Gln								tta Leu 1365				4223
										gaa Glu 1380				4268
		Ser				Ile				cag Gln 1395				4313
	-	Gln		-					-	gaa Glu 1410		-	gaa Glu	4358

	gaa Glu 1415					cag Gln 1420									4403
	cct Pro 1430					gac Asp 1435									4448
	cca Pro 1445	gaa Glu	caa Gln	agc Ser	aca Thr	tca Ser 1450	gaa Glu	aaa Lys	gca Ala	gta Val	tta Leu 1455	act Thr	tca Ser	cag Gln	4493
	agt Ser 1460	-	_			ata Ile 1465	_	_			-				4538
						tct Ser 1480									4583
						agg Arg 1495									4628
	gat Asp 1505					atg Met 1510									4673
	aga Arg 1520					caa Gln 1525									4718
	gag Glu 1535					gaa Glu 1540									4763
-	aca Thr 1550					agg Arg 1555									4808
	gaa Glu 1565					ctc Leu 1570						Glu			4853
	tct Ser 1580					cca Pro 1585									4898
	tct Ser 1595					ttg Leu 1600									4943
_	tct Ser 1610					gct Ala 1615									4988
999	tat	aat	gca	atg	gaa	gaa	agt	gtg	agc	agg	gag	aag	cca	gaa	5033

Gly	Tyr 1625	Asn	Ala	Met	Glu	Glu 1630	Ser	Val	Ser	Arg	Glu 1635	Lys	Pro	Glu	
	aca Thr 1640	gct Ala	tca Ser	aca Thr	gaa Glu	agg Arg 1645	gtc Val	aac Asn	aaa Lys	aga Arg	atg Met 1650	tcc Ser			5078
	tct Ser 1655					gaa Glu 1660									5123
	aga Arg 1670					act Thr 1675						act Thr	gaa Glu	gag Glu	5168
	act Thr 1685	cat His	gtt Val	gtt Val	atg Met	aaa Lys 1690	aca Thr	gat Asp	gct Ala	gag Glu	ttt Phe 1695	gtg Val	tgt Cys	gaa Glu	5213
						cta Leu 1705									5258
_	agc Ser 1715	Tyr	ttc Phe	tgg Trp	gtg Val	acc Thr 1720	cag Gln	tct Ser	att Ile	aaa Lys	gaa Glu 1725	aga Arg	aaa Lys	atg Met	5303
ctg Leu	aat Asn 1730	gag Glu	cat His	gat Asp	ttt Phe	gaa Glu 1735	gtc Val	aga Arg	gga Gly	gat Asp	gtg Val 1740	gtc Val	aat Asn	gga Gly	5348
_	aac Asn 1745	His	caa Gln	ggt Gly	cca Pro	aag Lys 1750	cga Arg	gca Ala	aga Arg	gaa Glu	tcc Ser 1755	cag Gln	gac Asp	aga Arg	5393
aag Lys	atc Ile 1760	Phe	agg Arg	Gly	cta Leu	gaa Glu 1765	atc Ile	tgt Cys	tgc Cys	tat Tyr	999 Gly 1770	ccc Pro	ttc Phe	acc Thr	5438
aac Asn	atg Met 1775	Pro	aca Thr	gat Asp	caa Gln	ctg Leu 1780	Glu	tgg Trp	atg Met	gta Val	cag Gln 1785	ctg Leu	tgt Cys	ggt Gly	5483
gct Ala	tct Ser 1790	Val	gtg Val	aag Lys	gag Glu	ctt Leu 1795	Ser	tca Ser	ttc Phe	acc Thr	ctt Leu 1800	Gly	aca Thr	ggt Gly	5528
gtc Val	cac His 1805	Pro	att Ile	gtg Val	gtt Val	gtg Val 1810	Gln	cca Pro	gat Asp	gcc Ala	tgg Trp 1815	aca Thr	gag Glu	gac Asp	5573
aat Asn	ggc Gly 1820	Phe	cat His	gca Ala	att Ile	999 Gly 1825	cag Gln	atg Met	tgt Cys	gag Glu	gca Ala 1830	Pro	gtg Val	gtg Val	5618
	cga Arg					gac Asp		gta Val	gca Ala	ctc Leu	tac Tyr	cag Gln	tgc Cys	cag Gln	5663

1845 1840 1835

5708

5711

gag ctg gac acc tac ctg ata ccc cag atc ccc cac agc cac tac Glu Leu Asp Thr Tyr Leu Ile Pro Gln Ile Pro His Ser His Tyr 1860 1855 tga <210> 268 <211> 1863 <212> PRT <213> Homo sapiens <400> 268 Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn 5 Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met 120 Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn 135 130 Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly 155 150 Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn 185 Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr

220

Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala

215

Ala 225	Cys	Glu	Phe	Ser	Glu 230	Thr	Asp	Val		Asn 235	Tnr	GIU	HIS		240
Pro	Ser	Asn	Asn	Asp 245	Leu	Asn	Thr	Thr	Glu 250	Lys	Arg	Ala	Ala	Glu 255	Arg
His	Pro	Glu	Lys 260	Tyr	Gln	Gly	Ser	Ser 265	Val	Ser	Asn	Leu	His 270	Val	Glu
Pro	Cys	Gly 275	Thr	Asn	Thr	His	Ala 280	Ser	Ser	Leu	Gln	His 285	Glu	Asn	Ser
Ser	Leu 290	Leu	Leu	Thr	Lys	Asp 295	Arg	Met	Asn	Val	Glu 300	Lys	Ala	Glu	Phe
Cys 305	Asn	Lys	Ser	Lys	Gln 310	Pro	Gly	Leu	Ala	Arg 315	Ser	Gln	His	Asn	Arg 320
Trp	Ala	Gly	Ser	Lys 325	Glu	Thr	Cys	Asn	Asp 330	Arg	Arg	Thr	Pro	Ser 335	Thr
Glu	Lys	Lys	Val 340	Asp	Leu	Asn	Ala	Asp 345	Pro	Leu	Cys	Glu	Arg 350	Lys	Glu
Trp	Asn	Lys 355	Gln	Lys	Leu	Pro	Cys 360	Ser	Glu	Asn	Pro	Arg 365	Asp	Thr	Glu
Asp	Val 370	Pro	Trp	Ile	Thr	Leu 375	Asn	Ser	Ser	Ile	Gln 380	Lys	Val	Asn	Glu
Trp 385	Phe	Ser	Arg	Ser	Asp 390	Glu	Leu	Leu	Gly	Ser 395	Asp	Asp	Ser	His	Asp 400
Gly	Glu	Ser	Glu	Ser 405	Asn	Ala	Lys	Val	Ala 410	Asp	Val	Leu	Asp	Val 415	Leu
Asn	Glu	Val	Asp 420		Tyr	Ser	Gly	Ser 425	Ser	Glu	Lys	Ile	Asp 430	Leu	Leu
Ala	Ser	Asp 435		His	Glu	Ala	Leu 440	Ile	Cys	Lys	Ser	Glu 445	Arg	Val	His
Ser	Lys 450		· Val	Glu	Ser	Asn 455		Glu	Asp	Lys	Ile 460	Phe	Gly	Lys	Thr
Tyr 465		Lys	Lys	Ala	Ser 470		Pro	Asn	. Leu	Ser 475	His	Val	Thr	Glu	Asn 480
Leu	Ile	: Ile	e Gly	Ala 485		· Val	Thr	Glu	Pro 490		Ile	Ile	: Gln	Glu 495	Arg
Pro	Leu	Thr	Asr 500		s Leu	. Lys	Arg	Lys 505		J Arg	Pro	Thr	510	Gly	Leu
His	Pro	Glu 515		Phe	e Ile	Lys	520	Ala	Asp	Leu	ı Ala	Val 525	Glr	Lys	Thr

Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp 550 Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys 565 570 Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser 580 585 Asn Met Glu Leu Glu Leu Asn Ile His Asn Ser Lys Ala Pro Lys Lys Asn Arg Leu Arg Arg Lys Ser Ser Thr Arg His Ile His Ala Leu Glu Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln 630 635 Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Tyr Asn 645 650 Gln Met Pro Val Arg His Ser Arg Asn Leu Gln Leu Met Glu Gly Lys 665 Glu Pro Ala Thr Gly Ala Lys Lys Ser Asn Lys Pro Asn Glu Gln Thr 680 Ser Lys Arg His Asp Ser Asp Thr Phe Pro Glu Leu Lys Leu Thr Asn . 695 Ala Pro Gly Ser Phe Thr Lys Cys Ser Asn Thr Ser Glu Leu Lys Glu Phe Val Asn Pro Ser Leu Pro Arg Glu Glu Lys Glu Glu Lys Leu Glu 725 730 Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ser Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His 805 Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro

825

820

- Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu 835 840 845
- Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser 850 855 860
- Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu 865 870 875 880
- Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser 885 890 895
- Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys 900 905 910
- Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly 915 920 925
- Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys 930 935 940
- Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly 945 950 955 960
- Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn 965 970 975
- Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr 980 985 990
- Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met 995
- Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val 1010 1015 1020
- Ser Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Glu 1025 1030 1035
- Ala Ser Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu 1040 1045 1050
- Val Gly Ser Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile 1055 1060 1065
- Gln Ala Glu Leu Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met 1070 1075 1080
- Leu Arg Leu Gly Val Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu 1085 1090 1095
- Pro Gly Ser Asn Cys Lys His Pro Glu Ile Lys Lys Gln Glu Tyr 1100 1105 1110
- Glu Glu Val Val Gln Thr Val Asn Thr Asp Phe Ser Pro Tyr Leu 1115 1120 1125